

SEQUENCE LISTING

78-0B10 amino acid sequence (SEQ ID NO:1)

5	Met	Ala	Asp	Lys	Asn	Ile	Leu	Tyr	Gly	Pro	Glu	Pro	Phe	Tyr	Pro	Leu
	1				5					10					15	
	Ala	Asp	Gly	Thr	Ala	Gly	Glu	Gln	Met	Phe	Asp	Ala	Leu	Ser	Arg	Tyr
			20					25						30		
	Ala	Asp	Ile	Ser	Gly	Cys	Ile	Ala	Leu	Thr	Asn	Ala	His	Thr	Lys	Glu
		35					40					45				
10	Asn	Val	Leu	Tyr	Glu	Glu	Phe	Leu	Lys	Leu	Ser	Cys	Arg	Leu	Ala	Glu
	50					55						60				
	Ser	Phe	Lys	Lys	Tyr	Gly	Leu	Lys	Gln	Asn	Asp	Thr	Ile	Ala	Val	Cys
	65				70					75					80	
	Ser	Glu	Asn	Gly	Leu	Gln	Phe	Phe	Leu	Pro	Val	Ile	Ala	Ser	Leu	Tyr
15				85						90					95	
	Leu	Gly	Ile	Ile	Ala	Ala	Pro	Val	Ser	Asp	Lys	Tyr	Ile	Glu	Arg	Glu
			100					105						110		
	Leu	Ile	His	Ser	Leu	Gly	Ile	Val	Lys	Pro	Arg	Ile	Ile	Phe	Cys	Ser
		115						120					125			
20	Lys	Asn	Thr	Phe	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Lys	Leu	Lys	Ser
	130					135						140				
	Val	Glu	Thr	Ile	Ile	Ile	Leu	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Gly	Tyr
	145				150					155						160
25	Gln	Cys	Leu	Asn	Asn	Phe	Ile	Ser	Gln	Asn	Ser	Asp	Ser	Asn	Leu	Asp
				165						170					175	
	Val	Lys	Lys	Phe	Lys	Pro	Tyr	Ser	Phe	Asn	Arg	Asp	Asp	Gln	Val	Ala
			180						185					190		
	Leu	Val	Met	Phe	Ser	Ser	Gly	Thr	Thr	Gly	Val	Pro	Lys	Gly	Val	Met
		195					200						205			
30	Leu	Thr	His	Lys	Asn	Ile	Val	Ala	Arg	Phe	Ser	Leu	Ala	Lys	Asp	Pro
	210					215						220				
	Thr	Phe	Gly	Asn	Ala	Ile	Asn	Pro	Thr	Thr	Ala	Ile	Leu	Thr	Val	Ile
	225				230					235					240	
35	Pro	Phe	His	His	Gly	Phe	Gly	Met	Met	Thr	Thr	Leu	Gly	Tyr	Phe	Thr
				245						250					255	
	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	His	Thr	Phe	Glu	Glu	Lys	Leu	Phe
			260					265					270			
	Leu	Gln	Ser	Leu	Gln	Asp	Tyr	Lys	Val	Glu	Ser	Thr	Leu	Leu	Val	Pro
		275					280						285			
40	Thr	Leu	Met	Ala	Phe	Leu	Ala	Lys	Ser	Ala	Leu	Val	Glu	Lys	Tyr	Asp
	290					295						300				
	Leu	Ser	His	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	Leu	Ser	Lys
	305				310					315					320	
45	Glu	Ile	Gly	Glu	Met	Val	Lys	Lys	Arg	Phe	Lys	Leu	Asn	Phe	Val	Arg
				325						330					335	
	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Val	Leu	Ile	Thr	Pro
			340					345					350			
	Lys	Gly	Asp	Ala	Arg	Pro	Gly	Ser	Thr	Gly	Lys	Ile	Val	Pro	Phe	His
		355					360						365			
50	Ala	Val	Lys	Val	Val	Asp	Pro	Thr	Thr	Gly	Lys	Ile	Leu	Gly	Pro	Asn
	370						375					380				
	Glu	Pro	Gly	Glu	Leu	Tyr	Phe	Lys	Gly	Ala	Met	Ile	Met	Lys	Gly	Tyr
	385				390					395					400	
55	Tyr	Asn	Asn	Glu	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asp	Asn	Asp	Gly	Trp
				405						410					415	

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35	Met	Ala	Asp	Lys	Asn	Ile	Leu	Tyr	Gly	Pro	Glu	Pro	Phe	Tyr	Pro	Leu
	1				5					10					15	
40	Glu	Asp	Gly	Thr	Ala	Gly	Glu	Gln	Met	Phe	Asp	Ala	Leu	Ser	Arg	Tyr
				20					25					30		
	Ala	Asp	Ile	Pro	Gly	Cys	Ile	Ala	Leu	Thr	Asn	Ala	His	Thr	Lys	Glu
			35					40					45			
45	Asn	Val	Leu	Tyr	Glu	Glu	Phe	Leu	Lys	Leu	Ser	Cys	Arg	Leu	Ala	Glu
	50						55					60				
	Ser	Phe	Lys	Lys	Tyr	Gly	Leu	Lys	Gln	Asn	Asp	Thr	Ile	Ala	Val	Cys
50	65				70					75					80	
	Ser	Glu	Asn	Ser	Leu	Gln	Phe	Phe	Leu	Pro	Val	Ile	Ala	Ser	Leu	Tyr
					85					90					95	
55	Leu	Gly	Ile	Ile	Val	Ala	Pro	Val	Asn	Asp	Lys	Tyr	Ile	Glu	Arg	Glu
				100					105					110		
	Leu	Ile	His	Ser	Leu	Gly	Ile	Val	Lys	Pro	Arg	Ile	Val	Phe	Cys	Ser
			115					120					125			
60	Lys	Asn	Thr	Phe	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Lys	Leu	Lys	Ser
		130					135					140				
	Ile	Glu	Thr	Ile	Ile	Ile	Leu	Asp	Leu	Asn	Asp	Asp	Leu	Gly	Gly	Tyr
	145					150					155				160	
65	Gln	Cys	Leu	Asn	Asn	Phe	Ile	Ser	Gln	Asn	Ser	Asp	Ser	Asn	Leu	Asp
					165					170					175	
70	Val	Lys	Lys	Phe	Lys	Pro	Tyr	Ser	Phe	Asn	Arg	Asp	Asp	Gln	Val	Ala
					180				185					190		

5	Leu	Ile	Met	Phe	Ser	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Gly	Val	Met
			195					200					205			
	Leu	Thr	His	Lys	Asn	Ile	Val	Ala	Arg	Phe	Ser	Ile	Ala	Lys	Asp	Pro
			210					215					220			
	Thr	Phe	Gly	Asn	Ala	Ile	Asn	Pro	Thr	Ser	Ala	Ile	Leu	Thr	Val	Ile
10	225						230					235				240
	Pro	Phe	His	His	Gly	Phe	Gly	Met	Met	Thr	Thr	Leu	Gly	Tyr	Phe	Thr
					245						250				255	
	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	His	Thr	Phe	Glu	Glu	Lys	Leu	Phe
				260						265				270		
15	Leu	Gln	Ser	Leu	Gln	Asp	Tyr	Lys	Val	Glu	Ser	Thr	Leu	Leu	Val	Pro
			275						280					285		
	Thr	Leu	Met	Ala	Phe	Leu	Ala	Lys	Ser	Ala	Leu	Val	Glu	Lys	Tyr	Asp
			290					295					300			
	Leu	Ser	His	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	Leu	Ser	Lys
20	305						310					315				320
	Glu	Ile	Gly	Glu	Met	Val	Lys	Lys	Arg	Phe	Lys	Leu	Asn	Phe	Val	Arg
					325						330				335	
	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Val	Leu	Ile	Thr	Pro
				340						345				350		
25	Lys	Gly	Asp	Ala	Lys	Pro	Gly	Ser	Thr	Gly	Lys	Ile	Val	Pro	Phe	His
			355					360					365			
	Ala	Val	Lys	Val	Val	Asp	Pro	Thr	Thr	Gly	Lys	Ile	Leu	Gly	Pro	Asn
			370					375					380			
	Glu	Pro	Gly	Glu	Leu	Tyr	Phe	Lys	Gly	Pro	Met	Ile	Met	Lys	Gly	Tyr
30	385						390					395				400
	Tyr	Asn	Asn	Glu	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asp	Asn	Asp	Gly	Trp
					405					410					415	
	Leu	Arg	Ser	Gly	Asp	Ile	Ala	Tyr	Tyr	Asp	Asn	Asp	Gly	His	Phe	Tyr
				420					425					430		
35	Ile	Val	Asp	Arg	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly	Tyr	Gln	Val
			435					440					445			
	Ala	Pro	Ala	Glu	Ile	Glu	Gly	Ile	Leu	Leu	Gln	His	Pro	Tyr	Ile	Val
			450				455						460			
	Asp	Ala	Gly	Val	Thr	Gly	Ile	Pro	Asp	Glu	Ala	Gly	Glu	Leu	Pro	
40	465						470					475				480
	Ala	Ala	Gly	Val	Val	Val	Gln	Thr	Gly	Lys	Tyr	Leu	Asn	Glu	Gln	Ile
					485					490					495	
	Val	Gln	Asp	Tyr	Val	Ala	Ser	Gln	Val	Ser	Thr	Ala	Lys	Trp	Leu	Arg
				500						505				510		
45	Gly	Gly	Val	Ile	Phe	Leu	Asp	Glu	Ile	Pro	Lys	Gly	Ser	Thr	Gly	Lys
			515					520					525			
	Ile	Asp	Arg	Lys	Val	Leu	Arg	Gln	Met	Leu	Glu	Lys	His	Thr	Asn	Gly
			530													

Met	Ala	Asp	Lys	Asn	Ile	Leu	Tyr	Gly	Pro	Glu	Pro	Phe	Tyr	Pro	Leu
1				5					10					15	
Glu	Asp	Gly	Thr	Ala	Gly	Glu	Gln	Met	Phe	Asp	Ala	Leu	Ser	Arg	Tyr
			20					25					30		
Ala	Ala	Ile	Pro	Gly	Cys	Ile	Ala	Leu	Thr	Asn	Ala	His	Thr	Lys	Glu
		35					40					45			
Asn	Val	Leu	Tyr	Glu	Glu	Phe	Leu	Lys	Leu	Ser	Cys	Arg	Leu	Ala	Glu
	50					55					60				
Ser	Phe	Lys	Lys	Tyr	Gly	Leu	Lys	Gln	Asn	Asp	Thr	Ile	Ala	Val	Cys
65					70					75					80

50	Met	Ala	Asp	Lys	Asn	Ile	Leu	Tyr	Gly	Ile	Glu	Ile	Ile	Tyr	Ile	Leu
	1				5					10					15	
	Glu	Asp	Gly	Thr	Ala	Gly	Glu	Gln	Met	Phe	Asp	Ala	Leu	Ser	Arg	Tyr
				20					25					30		
	Ala	Ala	Ile	Pro	Gly	Cys	Ile	Ala	Leu	Thr	Asn	Ala	His	Thr	Lys	Glu
			35					40					45			
55	Asn	Val	Leu	Tyr	Glu	Glu	Phe	Leu	Lys	Leu	Ser	Cys	Arg	Leu	Ala	Glu
	50						55					60				
	Ser	Phe	Lys	Lys	Tyr	Gly	Leu	Lys	Gln	Asn	Asp	Thr	Ile	Ala	Val	Cys
	65					70					75					80

	Ser	Glu	Asn	Ser	Leu	Gln	Phe	Phe	Leu	Pro	Val	Ile	Ala	Ser	Leu	Tyr
					85					90					95	
	Leu	Gly	Ile	Ile	Val	Ala	Pro	Val	Asn	Asp	Lys	Tyr	Ile	Glu	Arg	Glu
				100					105					110		
5	Leu	Ile	His	Ser	Leu	Gly	Ile	Val	Lys	Pro	Arg	Ile	Val	Phe	Cys	Ser
			115					120					125			
	Lys	Asn	Thr	Phe	Gln	Lys	Val	Leu	Asn	Val	Lys	Ser	Lys	Leu	Lys	Ser
		130					135					140				
10	Ile	Glu	Thr	Ile	Ile	Ile	Leu	Asp	Leu	Asn	Glu	Asp	Leu	Gly	Gly	Tyr
	145					150					155					160
	Gln	Cys	Leu	Asn	Asn	Phe	Ile	Ser	Gln	Asn	Ser	Asp	Ser	Asn	Leu	Asp
				165					170						175	
	Val	Lys	Lys	Phe	Lys	Pro	Tyr	Ser	Phe	Asn	Arg	Asp	Asp	Gln	Val	Ala
				180					185					190		
15	Ser	Ile	Met	Phe	Ser	Ser	Gly	Thr	Thr	Gly	Leu	Pro	Lys	Gly	Val	Met
			195				200						205			
	Leu	Thr	His	Lys	Asn	Ile	Val	Ala	Arg	Phe	Ser	Ile	Ala	Lys	Asp	Pro
		210					215					220				
20	Thr	Phe	Gly	Asn	Ala	Ile	Asn	Pro	Thr	Ser	Ala	Ile	Leu	Thr	Val	Ile
	225					230					235					240
	Pro	Phe	His	His	Gly	Phe	Gly	Met	Met	Thr	Thr	Leu	Gly	Tyr	Phe	Thr
					245					250					255	
	Cys	Gly	Phe	Arg	Val	Val	Leu	Met	His	Thr	Phe	Glu	Glu	Lys	Leu	Phe
				260					265					270		
25	Leu	Gln	Ser	Leu	Gln	Asp	Tyr	Lys	Val	Glu	Ser	Thr	Leu	Leu	Val	Pro
		275					280						285			
	Thr	Leu	Met	Ala	Phe	Leu	Ala	Lys	Ser	Ala	Leu	Val	Glu	Lys	Tyr	Asp
		290					295					300				
30	Leu	Ser	His	Leu	Lys	Glu	Ile	Ala	Ser	Gly	Gly	Ala	Pro	Leu	Ser	Lys
	305					310					315					320
	Glu	Ile	Gly	Glu	Met	Val	Lys	Lys	Arg	Phe	Lys	Leu	Asn	Phe	Val	Arg
					325					330					335	
	Gln	Gly	Tyr	Gly	Leu	Thr	Glu	Thr	Thr	Ser	Ala	Val	Leu	Ile	Thr	Pro
				340					345					350		
35	Lys	Gly	Asp	Ala	Lys	Pro	Gly	Ser	Thr	Gly	Lys	Ile	Val	Pro	Leu	His
			355					360					365			
	Ala	Val	Lys	Val	Val	Asp	Pro	Thr	Thr	Gly	Lys	Ile	Leu	Gly	Pro	Asn
		370					375					380				
40	Glu	Pro	Gly	Glu	Leu	Tyr	Phe	Lys	Gly	Pro	Met	Ile	Met	Lys	Gly	Tyr
	385					390					395					400
	Tyr	Asn	Asn	Glu	Glu	Ala	Thr	Lys	Ala	Ile	Ile	Asp	Asn	Asp	Gly	Trp
				405						410					415	
	Leu	Arg	Ser	Gly	Asp	Ile	Ala	Tyr	Tyr	Asp	Asn	Asp	Gly	His	Phe	Tyr
				420					425					430		
45	Ile	Val	Asp	Arg	Leu	Lys	Ser	Leu	Ile	Lys	Tyr	Lys	Gly	Tyr	Gln	Val
			435					440					445			
	Ala	Pro	Ala	Glu	Ile	Glu	Gly	Ile	Leu	Leu	Gln	His	Pro	Tyr	Ile	Val
		450					455					460				
50	Asp	Ala	Gly	Val	Thr	Gly	Ile	Pro	Asp	Glu	Ala	Ala	Gly	Glu	Leu	Pro
	465					470					475					480
	Ala	Ala	Gly	Val	Val	Gln	Thr	Gly	Lys	Tyr	Leu	Asn	Glu	Gln	Ile	
				485					490					495		
	Val	Gln	Asp	Tyr	Val	Ala	Ser	Gln	Val	Ser	Thr	Ala	Lys	Trp	Leu	Arg
			500						505					510		
55	Gly	Gly	Val	Lys	Phe	Leu	Asp	Glu	Ile	Pro	Lys	Gly	Ser	Thr	Gly	Lys
			515					520					525			
	Ile	Asp	Arg	Lys	Val	Leu	Arg	Gln	Met	Leu	Glu	Lys	His	Thr	Asn	Gly
		530					535						540			

78-0B10 (SEQ ID NO:5)
 GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCTTGGCTG
 ATGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGCAGATATTTCCGGA
 5 TGCATAGCATTGACAAATGCTCATACAAAAGAAAATGTTTATATGAAGAGTTTTTAAA
 ATTGTCGTGTCGTTTAGCGGAAAAGTTTTAAAAAGTATGGATTAAACAAAACGACACAA
 TAGCGGTGTGTAGCGAAAATGGTTTGCAATTTTTCCTTCCTGTAATTGCATCATTGTAT
 CTTGGAATAATTGCAGCACCTGTTAGTGATAAATACATTGAACGTGAATTAATACACAG
 TCTTGGTATTGTAAAACACGCATAATTTTTTGGCTCCAAGAATACTTTTCAAAAAGTAC
 10 TGAATGTAAAATCTAAATTAAAATCTGTAGAACTATTATTATATTAGACTTAAATGAA
 GACTTAGGAGGTATCAATGCCTCAACAACCTTTATTTCTCAAAATTCCGATAGTAATCT
 GGACGTAAAAAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTTGCGTTGGTAA
 TGTTTTCTTCTGGTACAACTGGTGTTCGAAGGGAGTCATGCTAACTCACAAGAATATT
 GTTGACGATTTTCTCTTGCAAAAGATCCTACTTTTGGTAACGCAATTAATCCACGAC
 15 AGCAATTTTAACGGTAATACCTTTCCACCATGGTTTTTGGTATGATGACCACATTAGGAT
 ACTTTACTTGTGGATTCCGAGTTGTTCTAATGCACACGTTTGAAGAAAACTATTTCTA
 CAATCATTACAAGATTATAAAGTGAAAGTACTTTACTTGTACCAACATTAATGGCATT
 TCTTGCAAAAAGTGCATTAGTTGAAAAGTACGATTTATCGCACTTAAAAGAAATTGCAT
 CTGGTGGCGCACCTTTATCAAAAGAAATTGGGGAGATGGTGAAAAAACGGTTTAAATTA
 20 AACTTTGTGAGGCAAGGGTATGGATTAACAGAAACCACTTCGGCTGTTTTAATTACACC
 GAAAGGTGACGCCAGACCGGGATCAACTGGTAAATAGTACCATTTCACGCTGTAAAG
 TTGTGCGATCCTACAACAGGAAAAATTTTGGGGCCAAATGAACCTGGAGAATTGTATTTT
 AAAGGCGCCATGATAATGAAGGGTATTATAATAATGAAGAAGCTACTAAAGCAATTAT
 TGATAATGACGGATGTTGCGCTCTGGTGATATTGCTTATTATGACAATGATGGCCATT
 25 TTTATATTGTGGACAGGCTGAAGTCATTAATTAATATAAAGGTTATCAGGTTGCACCT
 GCTGAAATTGAGGGAATACTCTTACAACATCCGTATATTGTTGATGCCGGCGTTACTGG
 TATACCGGATGAAGCCGCGGGCGAGCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGAA
 AATATCTAAACGAACAAATCGTACAAGATTTTGTTCAGTCAAGTTTCAACAGCCAAA
 TGGCTACGTGGTGGGGTGAATTTTGGATGAAATTTCCCAAAGGATCAACTGGAAAAAT
 30 TGACAGAAAAGTGTTAAGACAAATGTTTGAAAAACACACCAATGGG

90-1B5 (SEQ ID NO:6)
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 TGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGCAGATATTTCCGGGCTG 120
 35 CATAGCATTGACAAATGCTCATACAAAAGAAAATGTTTATATGAAGAGTTTCTGAAACT 180
 GTCGTGTCGTTTAGCGGAAAAGTTTTAAAAAGTATGGATTAAACAAAACGACACAATAGC 240
 GGTGTGTAGCGAAAATGGTCTGCAATTTTTCCTTCCTGTAATTGCATCATTGTATCTTGG 300
 AATAATTGTGGCACCTGTTAACGATAAATACATTGAACGTGAATTAATACACAGTCTTGG 360
 TATTGTAAAACACGCATAGTTTTTTGCTCCAAGAATACTTTTCAAAAAGTACTGAATGT 420
 40 AAAATCTAAATTAAATCTATTGAACTATTATTATATTAGACTTAAATGAAGACTTAGG 480
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 AAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTTGCGTTGATTATGTTTTCTTC 600
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 TTCTCTTGCAAAAGATCCTACTTTTGGTAACGCAATTAATCCCACGACAGCAATTTAAC 720
 45 GGTAATACCTTTCCACCATGGTTTTTGGTATGATGACCACATTAGGATACTTTACTTGTGG 780
 ATTCAGAGTTGTTCTAATGCACACGTTTGAAGAAAACTATTTCTACAATCATTACAAGA 840
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 50 GTATGGATTAAACAGAAACCACTTCGGCTGTTTTAATTACACCGAAAGGTGACGCCAAACC 1080
 GGGATCAACTGGTAAATAGTACCATTTCACGCTGTTAAAGTTGTCGATCCTACAACAGG 1140
 AAAAATTTTGGGGCCAAATGAACCTGGAGAATTGTATTTTAAAGGCCCGATGATAATGAA 1200

5 GGGTTATTATAATAATGAAGAAGCTACTAAAGCAATTATTGATAATGACGGATGGTTGCG 1260
 CTCTGGTGATATTGCTTATTATGACAATGATGGCCATTTTATATTGTGGACAGGCTGAA 1320
 GTCACCTGATTAAATATAAAGGTTATCAGGTTGCACCTGCTGAAATTGAGGGAATACTCTT 1380
 ACAACATCCGTATATTGTTGATGCCGGCGTTACTGGTATACCGGATGAAGCCGCGGGCGA 1440
 GCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGAAAATATCTAAACGAACAAATCGTACA 1500
 AGATTATGTTGCCAGTCAAGTTTCAACAGCCAAATGGCTACGTGGTGGGGTGAAATTTTT 1560
 GGATGAAATTCCCAAAGGATCAACTGGAAAATTGACAGAAAAGTGTTAAGACAAATGTT 1620
 TGAAAAACACACCAATGGG 1639

10 133-1B2 (SEQ ID NO:7)
 AGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCTTGGAAG
 ATGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGCAGATATTCGGGGC
 TGCATAGCATTGACAAATGCTCATACAAAAGAAAATGTTTTATATGAAGAGTTTCTGAA
 ACTGTCGTGTCGTTTAGCGGAAAGTTTTAAAAAGTATGGATTA AAAACAAAACGACACAA
 15 TAGCGGTGTGTAGCGAAAATAGTCTGCAATTTTTCTTCCTGTAATTGCATCATTGTAT
 CTTGGAATAATTGTGGCACCTGTTAACGATAAATACATTGAACGTGAATTAATACACAG
 TCTTGATTATTGTA AAAACCACGCATAGTTTTTTGCTCCAAGAATACTTTTCAAAAAGTAC
 TGAATGTAAAATCTAAATTAAAATCTATTGAAACTATTATTATATTAGACTTAAATGAT
 GACTTAGGAGGTTATCAATGCCTCAACAACCTTTATTTCTCAAAATTCGATAGTAATCT
 20 GGACGTAAAAAAATTTAAACCATATTCTTTTAATCGAGACGATCAGGTTGCGTTGATTA
 TGTTCCTCTGTTGTAACAAGTCTGCGGAAGGGAGTCATGCTAACTCACAAGAATATT
 GTTGCACGATTTTCTATTGCAAAAAGATCCTACTTTTGGTAACGCAATTAATCCACGTC
 AGCAATTTTAAACGGTAATACCTTTCCACCATGGTTTTTGGTATGATGACCACATTAGGAT
 ACTTTACTTGTGGATTCCGAGTTGTTCTAATGCACACGTTTGAAGAAAAACTATTTCTA
 25 CAATCATTACAAGATTATAAAGTGGAAGTACTTTACTTGTACCAACATTAATGGCATT
 TCTTGCAAAAAGTGCAATTAGTTGAAAAGTACGATTTTATCGCACTTAAAAGAAATTGCAT
 CTGGTGGCGCACCTTTATCAAAAAGAAATTTGGGGAGATGGTGAAAAAACGGTTTAAATTA
 AACTTTGTGAGGCAAGGGTATGGATTAACAGAAACCACCTTCGGCTGTTTAAATTACACC
 30 GAAAGGTGACGCCAAACCGGGATCACTGGTAAAATAGTACCATTTACGCTGTAAAG
 TTGTCGATCCTACAACAGGAAAAATTTTGGGGCCAAATGAACCTGGAGAATTGTATTTT
 AAAGGCCCCGATGATAATGAAGGGTTATTATAATAATGAAGAAGCTACTAAAGCAATTAT
 TGATAATGACGGATGGTTGCGCTCTGGTGATATTGCTTATTATGACAAATGATGGCCATT
 TTTATATTGTGGACAGGCTGAAGTCACTGATTAAATATAAAGGTTATCAGGTTGCACCT
 GCTGAAATTGAGGGAATACTCTTACAACATCCGTATATTGTTGATGCCGGCGTTACTGG
 35 TATACCGGATGAAGCCGCGGGCGAGCTTCCAGCTGCAGGTGTTGTAGTACAGACTGGAA
 AATATCTAAACGAACAAATCGTACAAGATTATGTTGCCAGTCAAGTTTCAACAGCCAAA
 TGGCTACGTGGTGGGGTGATATTTTTGGATGAAATTCCCAAAGGATCAACTGGAAAAAT
 TGACAGAAAAGTGTTAAGACAAATGTTAGAAAAACACACCAATGGG

40 146-1H2 (SEQ ID NO:8)
 GGATCCAATGGCAGATAAGAATATTTTATATGGGCCCCGAACCATTTTATCCCTTGGAAG
 ATGGGACGGCTGGAGAACAGATGTTTGACGCATTATCTCGTTATGCAGCTATTCGGGGC
 TGCATAGCATTGACAAATGCTCATACAAAAGAAAATGTTTTATATGAAGAGTTTCTGAA
 ACTGTCGTGTCGTTTAGCGGAAAGTTTTAAAAAGTATGGATTA AAAACAAAACGACACAA
 45 TAGCGGTGTGTAGCGAAAATAGTCTGCAATTTTTCTTCCTGTAATTGCATCATTGTAT
 CTTGGAATAATTGTGGCACCTGTTAACGATAAATACATTGAACGTGAATTAATACACAG
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